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Indicator taxa of spider (*Araneae*) diversity and their efficiency in conservation

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Abstract

A considerable number of alternative approaches have been suggested during the last years to predict species richness of a given taxon, while retaining information on the identities of the observed individuals. Such information can be extremely useful for choosing conservation priority areas, either by using raw richness values or, preferentially, by considering the complementarity between potential sites. Among the most popular approaches is the use of indicator taxa. Both one single family and a group of several families are here tested in their ability to predict the number of spider (*Araneae*) species independently of sampling effort, geographical location and type of habitat. We use data from three Portuguese protected areas as a test case. A two-family indicator group – Gnaphosidae and Theridiidae – is found to be a good surrogate of species richness, even if caution is needed regarding the comparison of sites with considerably different sampling effort or vegetation cover. No single family can be seen as a good surrogate of the totality of spiders. In addition, only a group of the two mentioned families is found to be efficient and reliable either when used to rank sites according to taxa richness or for determining near-minimum sets of sites for conservation. We therefore recommend surrogacy with this indicator group as a promising approach for the prediction of spider species richness or evaluation and ranking of areas according to their conservation importance. The reached conclusions should uphold for Portugal and the entire Mediterranean region.
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Keywords: Species richness; Estimation; Complementarity; Portugal; Mediterranean

1. Introduction

A considerable number of alternative approaches have been suggested during the last years to predict the number of species encompassed by any given taxon when not all of them are known and to infer on the spatial and temporal distribution of biodiversity. Such approaches try to overcome the problem of the enormous amount of resources (e.g. time, money, taxonomists) required to reach complete inventories, if such goal is ever possible to achieve. Among the most popular is the use of indicator taxa whose diversity values shall ideally reflect overall diversity, whatever the taxon or spatial scale we want to apply surrogacy data (e.g. Pearson and Cassola, 1992; Beccaloni and Gaston, 1995; Duelli and Obrist, 1998). Alternative (or maybe complementary) approaches are the use of higher taxa surrogates (e.g. Gaston and Williams, 1993; Williams and Gaston, 1994; Balmford et al., 2000; Cardoso et al., 2004) and the inference of diversity from available information on environmental variables (e.g. Braithwaite et al., 1989; McNally et al., 2003).

The raw number of represented species is certainly not the ideal figure for conservation decisions, their rarity, phylogenetic diversity, persistence probabilities and a number of other factors can be taken into account. However, such values are often not possible to obtain and, despite all the pros and cons all the above

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approaches have, surrogate information on the number of species is all we can achieve. The indicator taxa approach has several advantages over other methods, namely by allowing obtaining very precise and complete information on the considered taxa with relatively low effort and resource use. Another crucial advantage is the retention of broad biological information that allows the understanding of distribution patterns and more efficiency in the definition of areas suitable for species conservation (Pearson and Cassola, 1992; Ryti, 1992; Faith and Walker, 1996; Prendergast and Eversham, 1997; Van Jaarsveld et al., 1998; Reyers et al., 2000). Although some of previous work points to a reliable use of indicator taxa as surrogates in many different kinds of organisms (Pearson and Cassola, 1992; Beccaloni and Gaston, 1995; Duelli and Obrist, 1998; Reyers et al., 2000), this approach has failed in other cases (Prendergast et al., 1993; Prendergast and Eversham, 1997; Lawton et al., 1998; Van Jaarsveld et al., 1998) mainly due to the use of many unrelated and ecologically diverse taxa that do not behave similarly with habitat or geographical change. Like with higher taxa surrogacy, caution is mandatory, given that several factors may influence the relationship between overall species richness and indicator taxa richness. Some of these factors are sampling effort, geographical location and habitat type (Gaston and Williams, 1993; Andersen, 1995; Cardoso et al., 2004).

Spider species richness and respective spatial distribution are virtually unknown in Portugal (Cardoso, 2000, 2004). Although no single family data is available for most of the country's territory, given the difficulty in the identification of species, many remaining to be described or discovered, it seems advisable to test for future use such potential tools as are different surrogates of biodiversity.

The higher taxa approach has been recently tested with the same dataset and methodology here applied, with very good results (Cardoso et al., 2004). With this work, we intend to provide evidence of usefulness of the indicator taxa approach with spiders in Portugal and the entire Mediterranean region, using it for overall richness prediction and definition of conservation priority areas. The comparison between these two approaches is also one of the issues to be discussed.

2. Methods

2.1. Fieldwork

Fieldwork design was implemented to test for several effects that can influence the indicator taxa approach – geographical location, type of habitat and sampling effort. Three Portuguese protected areas were chosen, one in the north – Douro Internacional Natural Park –

sampled during 2001, and two nearby areas closer to the south of the country – Serras de Aire e Candeeiros Natural Park and Paúl do Boquilobo Nature Reserve – sampled during 2002 (Fig. 1). For a question of simplicity, these three areas are simply referenced from now on as belonging to north and south geographical regions since the latter two are very close to each other. Ideally, all sites in all protected areas should have been sampled during the same year, but the distance between them and the large number of sites involved made it logistically unfeasible. We chose such areas due to high habitat diversity and, by comparing the two regions, allowing the study of geographical effects on the surrogacy methods to be tested (Table 1). In each area, we sampled several sites, summing 27, trying to cover the majority of the most significant habitats represented. This way, we could also consider habitat effect by differentiating sites with and without arboreal cover and those with "natural", autochthonous vegetation, from the ones dominated by introduced vegetation or under severe human influence or management. To test for sampling effort
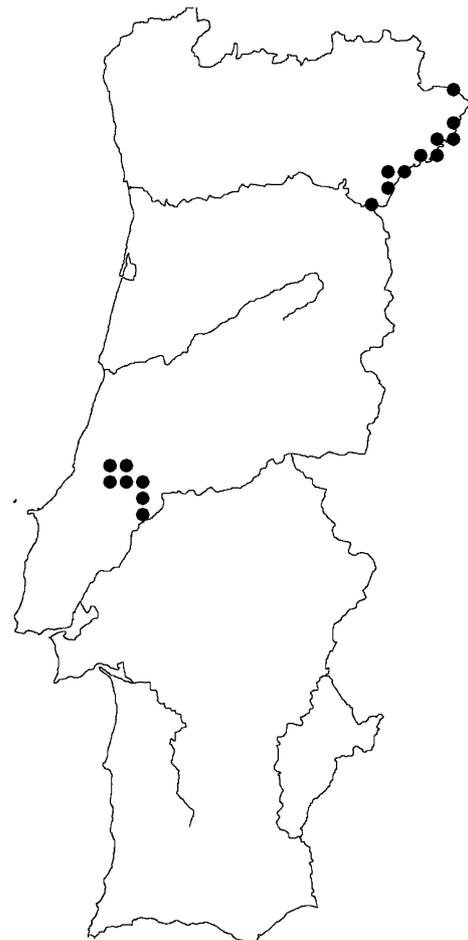

Fig. 1. Location of sampled sites in Portugal according to UTM squares (10 × 10 km). A single circle can refer to different sites if they are located at the same square.

Table 1
Sampled sites with respective code, Universal Transverse Mercator square (10 × 10 km) and characteristics: sampling effort (High or Low), location in the country (North or South), presence of arboreal vegetation (Yes or No) and "naturalness" of the habitat (Natural or Human influenced)

Site	Code	UTM	Effort	Location	Arboreal	Natural
Paúl Boquilobo (montado)	PBM	29SND36	H*	S	Y	H
Fonte d'Aldeia	FAM	29TQF18	H	N	Y	H
Palão	PAE	29TPF85	H	N	Y	H
Mazouco	MAG	29TPF85	H	N	N	N
Algozinho	ALR	29TQF07	H	N	Y	N
Tó	TOC	29TQF07	H	N	Y	N
Vila Chã da Braciosa	VCP	29TQF28	H	N	N	H
Picotino	PIP	29TPF86	H	N	Y	H
Vale Garcia	VGM	29SND37	H	S	N	N
Serro Ventoso	SVC	29SND17	H	S	Y	N
Barrenta	BAE	29SND28	H	S	Y	H
Picote	PIM	29TQF28	L	N	Y	N
Bruçó	BRP	29TPF96	H	N	Y	H
Bairro	BAP	29SND37	H	S	Y	H
Picote (arribas)	PIR	29TQF28	H	N	N	N
Mira d'Aire	MIP	29SND27	H	S	N	H
Freixiosa	FRA	29TQF29	L	N	Y	N
Constantim	COC	29TQG21	L	N	Y	N
Paúl Boquilobo (valas)	PBV	29SND36	L	S	Y	N
Paúl Boquilobo (choupal)	PBC	29SND36	L	S	Y	H
Paúl Boquilobo (salgueiral)	PBS	29SND35	H	S	Y	N
Bemposta	BEZ	29TQF17	L	N	Y	N
Barca d'Alva	BAM	29TPF74	L	N	N	N
Lagoaça	LAC	29TPF96	L	N	Y	N
Santo António	SÃO	29SND27	L	S	N	H
Lamoso	LAR	29TQF07	L	N	Y	N
Sao Mamede	SMM	29SND18	L	S	N	N

* Very high effort, not comparable to other sites.

influence over surrogacy results, some of the sites were subjected to high effort, others to low effort sampling. High effort consisted in a 10-month continuous sampling, from February to November. A row of eight 33 cl capacity pitfall traps, each 5 m apart from the next in line was set up for each site. We used beer cups with 8 cm diameter and 12 cm depth during the all 10-month period, with fortnightly collecting. Sweep netting sessions with the duration of 1 h were performed only once, in the end of May or beginning of June, at each site with a standard 40 cm diameter sweep net. Low effort sites were sampled in the same way as high effort, except for the sampling period duration, as we made one single month pitfall trapping during May and June, with one sweep netting session during the middle of that period. One of the sites (PBM) suffered from a very intensive collecting effort, with 10 month continuous pitfall trapping with 32 traps and sweep netting sessions of 1 h every two weeks during the all period.

2.2. Statistical procedures

Only adults were considered for computation, given that juveniles are almost invariably impossible to identify. To test if either one family or a group of families of spiders can be reliably used to predict overall observed spider species richness, we performed linear regression analysis over all available data. We used both the percentage of variance explained by the independent variable (r^2) and visual evaluation of the scatter plots as a measure of adjustment, surrogacy reliability and predictive power. To test for the possible influence of sampling effort, geographical location and habitat type over surrogacy results, we also adjusted regression lines after separating sites according to their characteristics, one factor at a time. We used analysis of covariance (ANCOVA) in order to test for statistically significant differences between regression lines. If differences were found, the factor involved was considered as potentially influencing the reliability of surrogacy. Statistica 5.1 software was used for statistical analysis (Statsoft Inc., 1998). For allowing a reliable analysis of covariance, we had to exclude PBM, since it can be considered as an outlier, not possible to compare with other sites, all of them having a much lower sampling effort. Its inclusion would only change regression and covariance in artificial and unpredictable ways.

Two approaches were tested for prioritisation and ranking of sites for conservation. First, a scoring approach, which uses the raw number of species represented in each site as the sole value for ranking. We used Spearman rank correlation index to test for surrogacy

reliability in the scoring of sites. In addition, scatter plots of one and several families' richness versus overall species richness ranking of sites were used for visual inspection of reliability. Secondly, we tested a more efficient iterative approach of conservation priority ranking. For each of the considered taxa (one family, several families or all families), we first chose the richest site and from it, in a stepwise manner, the one site that would further raise the number of represented species was added to the set of sites to be considered for protection. In case of ties, we chose the most species rich site in the respective taxa. By doing so, we could test the effect of using indicator taxa for choosing a near-minimum set of sites that potentially preserves the maximum number of spider species.

3. Results

About 30,000 spiders, 16,951 adults included, belonging to 412 species or morphospecies were captured during the entire two years fieldwork. Morphospecies have to be consistently used in many cases in Portugal and the Mediterranean due to the high proportion of undescribed species. In this case, it was only possible for us to identify about two-thirds of the species, even with the help of many experts of different families. We will now refer to all of them as species, independently of having been identified or not. The 412 species belong to 162 identified genera and 39 families. All numbers are considerably high compared to the known fauna of 693 species, 250 genera and 45 families currently registered for Portugal, which should still be very far from the real numbers (Cardoso, 2000, 2004). The most represented families were Gnaphosidae (73 species), Linyphiidae (71), Theridiidae (41), Salticidae (33), Thomisidae (24), Lycosidae (17), Araneidae (16), Agelenidae (13), Philodromidae (12), Dysderidae (11), and Dictynidae (10). Adopted systematics consistently follows Platnick's world spider catalog (2004).

3.1. Species richness prediction

3.1.1. Choosing the best surrogate

After fitting linear regression to all 39 families, we find Gnaphosidae to have, by far, the highest relationship value with overall spider richness, presenting a regression coefficient of 76% (Table 2; Fig. 2(a)). This family presents a highly significant relationship with the total number of species ($n = 27$, $p < 0.001$). However, a highly significant relationship does not equal to high predictive power (Andersen, 1995; Cardoso et al., 2004). We verify that some sites with similar number of gnaphosids have very different numbers of all species (Table 3; Fig. 2(a)).

Table 2
Accumulation of families in the indicator group, according to the one that most rises the regression coefficient at each step

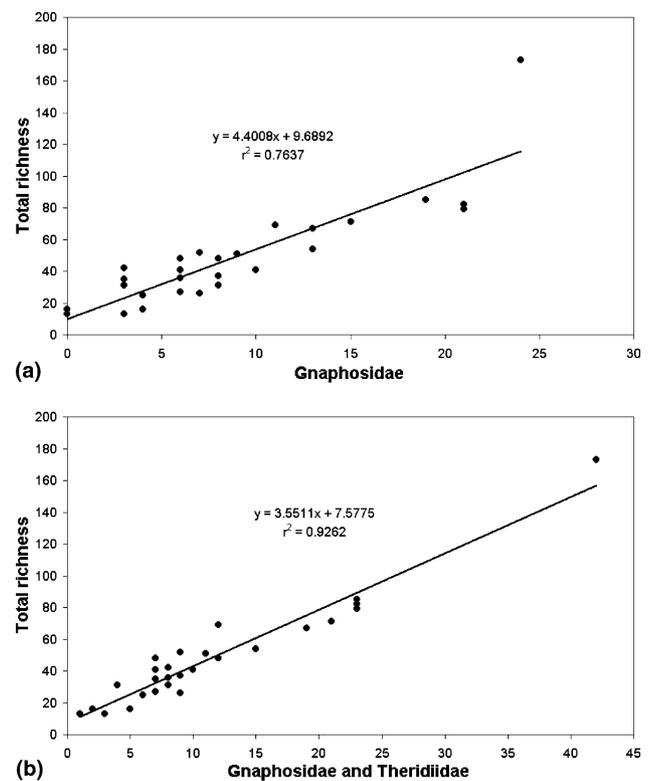| No. families	Family added at each step	Cumulative number of species	Regression coefficient (r^2)
1	Gnaphosidae	73	0.764
2	Theridiidae	114	0.926
3	Dysderidae	125	0.955
4	Tetragnathidae	133	0.969
5	Anyphaenidae	137	0.973
6	Uloboridae	139	0.977
7	Sparassidae	142	0.978
8	Pisauridae	143	0.979
9	Segestriidae	145	0.980
10	Corinnidae	153	0.982

Fig. 2. (a) Linear relationship between Gnaphosidae and total species richness in all 27 sampled sites. (b) Linear relationship between a two-family indicator group and total species richness in all 27 sampled sites (some of the circles are overlapping).

Correspondingly, sites with similar number of all species present very different numbers of gnaphosids. In addition, the site with the highest sampling effort (PBM) presents very distant richness values from what would be expected (Fig. 2(a)). We then start adding families according to the one that, at each step, will most increase the regression coefficient value. We perform it up to nine times, until reaching a group of 10 families (Table 2). More than these and the group would become so large that surrogacy advantages over the identification of the totality of species would be lost. Right after

Table 3
Taxa richness of sampled sites and respective ranking

Site	Richness			Ranking		
	Gnaphosidae	Gnaphosidae and Theridiidae	Total	Gnaphosidae	Gnaphosidae and Theridiidae	Total
PBM	24	42	173	1	1	1
FAM	19	23	85	4	2	2
PAE	21	23	82	2	2	3
MAG	21	23	79	2	2	4
VCP	15	21	71	5	5	5
ALR	11	12	69	8	8	6
TOC	13	19	67	6	6	7
VGM	13	15	54	6	7	8
SVC	7	9	52	14	12	9
PIP	9	11	51	10	10	10
PIM	8	12	48	11	8	11
BAE	6	7	48	16	18	11
BRP	3	8	42	22	15	13
PIR	10	10	41	9	11	14
BAP	6	7	41	16	18	14
MIP	8	9	37	11	12	16
COC	6	8	36	16	15	17
FRA	3	7	35	22	18	18
PBV	8	8	31	11	15	19
PBS	3	4	31	22	24	19
PBC	6	7	27	16	18	21
BEZ	7	9	26	14	12	22
BAM	4	6	25	20	22	23
SAO	4	5	16	20	23	24
LAC	0	2	16	26	26	24
SMM	3	3	13	22	25	26
LAR	0	1	13	26	27	26

the first step, when theridiids are added, the regression coefficient becomes greater than 92% and the scatter plot does not present any large incongruence (Table 2, Fig. 2(b)). Despite being two of the most species rich families, Gnaphosidae and Theridiidae only represent 28% of all species in the dataset, but they can provide us with reliable estimates of the total number of spider species present at any site. Therefore, the adding of more families to the possible indicator group does not seem to be necessary, it would only increase effort without the correspondent increase in the reliability of estimates.

3.1.2. Influence of factors

Since we reached a group of two families as being the most reliable and efficient indicator group, with high predictive power of overall species richness, we only test the influence of several factors for this possible two-family group. Comparing regression lines of sites presenting different sampling effort (Fig. 3(a)), we find them to be highly significantly different ($n = 26$, $p < 0.001$). This is caused by the fact that these families are particularly easy to collect with the employed methodology and the more we collect, the more we start capturing species from other, not so easily collected, families. The

same does not happen with differences between northern and southern sites, whose regression lines are equal ($n = 26$, n.s.) (Fig. 3(b)). Habitat, however, may influence surrogacy reliability. There are differences between sites with and without tree cover ($n = 26$, $p < 0.05$). Fig. 3(c) suggests that the two families represent a higher proportion, relative to other families, at sites without arboreal vegetation (see also Table 3). The last tested effect, naturalness of the habitat, is not found to have any influence on surrogacy results ($n = 26$, n.s.) (Fig. 3(d)).

3.2. Conservation priority

3.2.1. Scoring approach

Using the rank of sites according to their taxa richness, we find Gnaphosidae alone to have low predictive power of all-species-based site ranking (Table 3), despite the high Spearman rank correlation value of 0.861. Examination of the rank scatter plot (Fig. 4(a)) also leads us to conclude about the low reliability of the single-family approach. The two-family indicator group, on the contrary, seems to rank sites much closer to overall species ranking (Table 3) (Spearman rank correlation = 0.914). Predictive power is especially high at
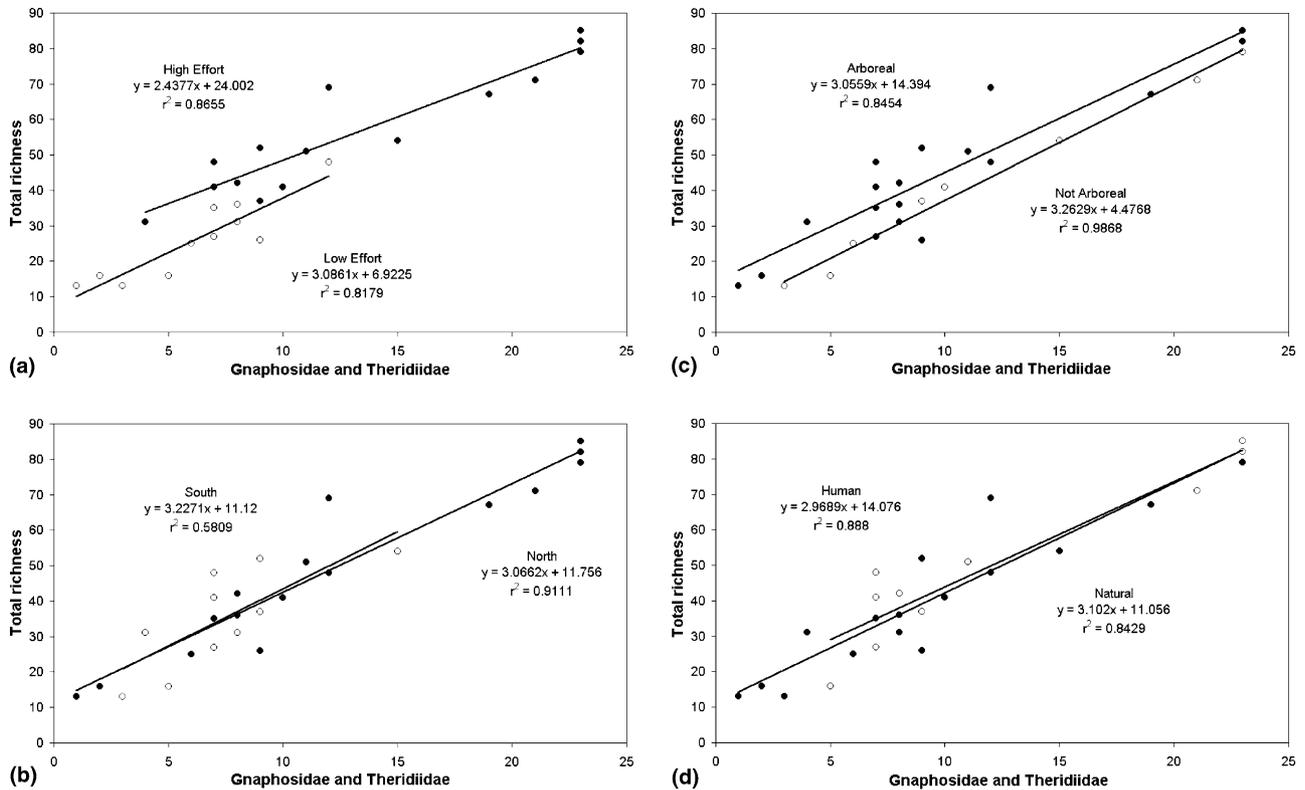
Fig. 3. (a) Comparison of indicator group richness and total species richness relationship between high (filled circles) and low (open circles) effort sites. (b) Comparison of indicator group richness and total species richness relationship between northern (filled circles) and southern (open circles) sites. (c) Comparison of indicator group richness and total species richness relationship between sites with (filled circles) and without (open circles) arboreal cover. (d) Comparison of indicator group richness and total species richness relationship between sites considered as "natural" (filled circles) and those with high human influence (open circles).

the highest ranked sites, being not as good at the middle and lower ones (Fig. 4(b)).

3.2.2. Iterative approach

Although a scoring approach to site ranking can be evaluated for future use, it is not the most efficient method for establishing conservation networks of sites. Complementarity is a fundamental issue to take into account. This way, we should score sites not according to their richness values, but according to which ones will allow the protection of the maximum number of species not included in previously chosen sites. By using accumulation curves, we can see the effects of adopting this approach for the different possible indicator taxa (Fig. 5). The objective is to check what proportion of total spider species can be protected by using the same number of sites that protects all species belonging to the tested taxa. Twenty four (89%) sites are necessary to include total species richness but only 21 (78%) for gnaphosids and theridiids and 12 (44%) for gnaphosids alone. The number of sites necessary to include all the gnaphosids is enough to protect, at most, 90% of species. If both gnaphosids and theridiids are used, close to 99% of species belonging to all families can be protected with the same number of sites.

4. Discussion

Previously in Portugal, a slightly larger group of families (Gnaphosidae, Lycosidae, Theridiidae and Agelenidae) has been appointed as the best to use as surrogate, although such analyses were limited to the Northern area of the study now presented (Cardoso et al., in press). Given the effort employed in pitfall trapping, three of those four families are mainly represented by ground dwelling species. The inclusion of the Southern areas came to increase the relative importance of theridiids, mainly due to the site PBM, in which we also performed intensive sweeping. As a final result, we ended up with only two families as the most important to identify to species level, the mainly epigeal gnaphosids and the mainly non-epigeal theridiids. Even if we had a considerably increased effort directed towards non-epigeal spiders these two should remain as the chosen. Moreover, epigeal spiders possible to capture with pitfall trapping have been found to make up close to half the species present in a typical Mediterranean habitat, being this the most efficient of a variety of commonly employed methods (Cardoso et al. in preparation, a, b). All these considerations taken into account, all data points to the fact that only a group of two families, Gnaphosidae and
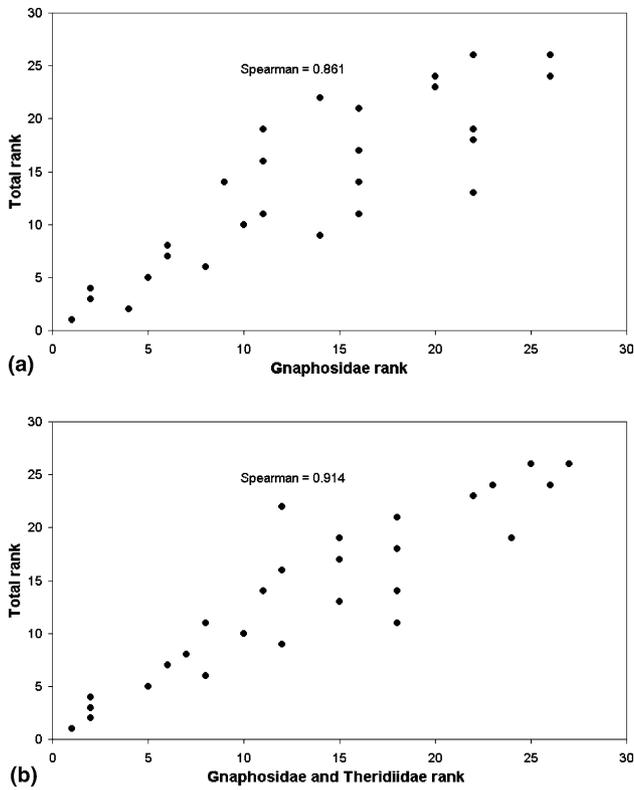
Fig. 4. (a) Comparison of site ranking according to Gnaphosidae and total species richness. (b) Comparison of site ranking according to two-family indicator group and total species richness.
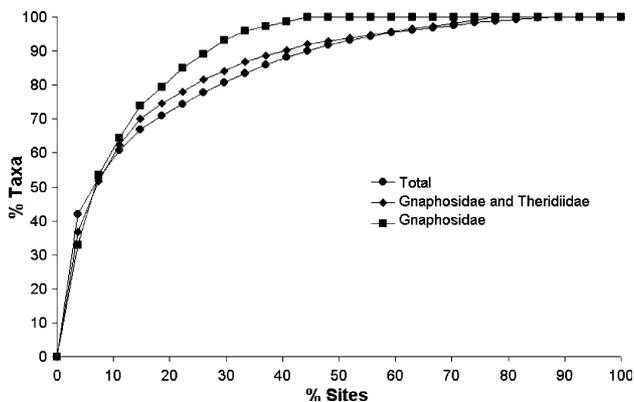

Fig. 5. Accumulation curves of the number of species represented by the adding of sites in a stepwise manner, considering complementarity.

Theridiidae, can be used as a significant and reliable surrogate of overall species richness in Portugal and the Mediterranean region, with much higher relationship value and predictive power than any single family. Of course, in other regions of the world, different families can be considered as better indicators (e.g. Marusik and Koponen, 2002). Nevertheless, two factors should be considered, sampling effort and the existence or not of arboreal vegetation, which can influence the reliability of predictions and difficult comparisons between sites with different characteristics. Neither geographical location or habitat naturalness are found to have significant influ-

ence over the usefulness of surrogacy. However, other surrogacy approach, using genera as higher taxa surrogates, can provide more precise estimates of species richness of spiders in Portugal, with less potentially influencing factors (Cardoso, 2004).

Using a group of the two above-mentioned families is also found to be a good way for choosing priority sites for conservation. Either if we choose to apply a simple scoring approach or a much more efficient iterative approach to the problem of sites ranking, this indicator group can be used as a surrogate of all spiders, when no data is available on these. Some caution should be used, though, and in case of doubt a conservative approach should be taken, by trying to protect more sites than those expected to be necessary to represent all species from the indicator taxa. This way we should be able to guarantee that the proposed reserve network covers a large proportion of all spider species. Contrary to what happens with species richness estimates, the indicator taxa approach used for choosing conservation priority areas, is even more efficient than the use of genera surrogacy with the same dataset (Cardoso et al., 2004), at least if an iterative algorithm is used.

However, two questions may refrain our enthusiasm regarding the use of gnaphosids and theridiids as surrogates of all spiders. First, possible loosing of more information happens when compared to higher taxa surrogacy. Second, this approach requires the identification of all species belonging to the surrogate taxa, which is many times difficult. In our dataset, they represent 28% of overall spider species richness. However, higher taxa surrogacy has its own problems like constant changing of systematics of all invertebrates, particularly spiders (Platnick, 2004), and the difficulty of identifying many individuals even to genus level, what is related to the previous issue (Cardoso et al., 2004). Moreover, the use of indicator taxa also has the advantage that all morphospecies, even if not identified to genera level, can be considered. Despite some problems inherent to this approach, our work concludes that not only it is a reliable but also an extremely useful method for both species richness prediction and definition of a conservation priority sites network. Surrogacy can be seen as both a preliminary approach, if not possible to have all species identified in a reasonable amount of time for conservation purposes, or an end in itself, in regions where most species are unknown, or when no resources are available to identify all species belonging to all families.

Acknowledgements

References

Andersen, A.N., 1995. Measuring more of biodiversity: genus richness as a surrogate for species richness in Australian ant faunas. Biological Conservation 73, 39–43.

Balmford, A., Lyon, A.J.E., Lang, R.M., 2000. Testing the higher-taxon approach to conservation planning in a megadiverse group: the macrofungi. Biological Conservation 93, 209–217.

Beccaloni, G.W., Gaston, K.J., 1995. Predicting the species richness of neotropical forest butterflies: Ithomiinae (Lepidoptera: Nymphalidae) as indicators. Biological Conservation 71, 77–86.

Braithwaite, L.W., Austin, M.P., Clayton, M., Turner, J., Nicholls, A.O., 1989. On predicting the presence of birds in Eucalyptus forest types. Biological Conservation 50, 33–50.

Cardoso, P., 2000. Portuguese spiders (*Araneae*): a preliminary checklist. In: Gajdos, P., Pekár, S. (Eds.), Proceedings of the 18th European Colloquium of Arachnology. Ekológia (Bratislava) vol. 19, pp. 19–29.

Cardoso, P., 2004. Portugal spider checklist. Available online at: <http://www.geocities.com/rainforest/vines/5197/checklist.html>.

Cardoso, P., Silva, I., de Oliveira, N.G., Serrano, A.R.M., 2004. Higher taxa surrogates of spider (*Araneae*) diversity and their efficiency in conservation. Biological Conservation 117, 453–459.

Cardoso, P., de Oliveira, N.G., Silva., I, Serrano, A.R.M. Higher taxa surrogates versus surrogate groups of spider biodiversity. In: Samu, F. Szinetár, C. (Eds.), Proceedings of the 20th European Colloquium of Arachnology. European Arachnology 2002, (in press).

Cardoso, P., Gaspar, C., Silva, I., Pereira, L.C. A first proposal for a spider inventory protocol in a typical Mediterranean habitat (in preparation a).

Cardoso, P., Silva, I., Gaspar, C., Pereira, L.C. Comparison of strategies for the inventory of spiders (*Araneae*) in a typical Mediterranean habitat (in preparation b).

Duelli, P., Obrist, M.K., 1998. In search of the best correlates for local organismal biodiversity in cultivated areas. Biodiversity and Conservation 7, 297–309.

Faith, D.P., Walker, P.A., 1996. How do indicator groups provide information about the relative biodiversity of different sets of areas?: on hotspots, complementarity and pattern-based approaches. Biodiversity Letters 3, 18–25.

Gaston, K.J., Williams, P.H., 1993. Mapping the world's species – the higher taxon approach. Biodiversity Letters 1, 2–8.

Lawton, J.H., Bignell, D.E., Bolton, B., Bloemers, G.F., Eggleton, P., Hammond, P.M., Hodda, M., Holt, R.D., Larsen, T.B., Mawdsley, N.A., Stork, N.E., Srivastava, D.S., Watt, A.D., 1998. Biodiversity inventories, indicator taxa and effects of habitat modification in tropical forest. Nature 391, 72–76.

McNally, R., Fleishman, E., Fay, J.P., Murphy, D.D., 2003. Modelling butterfly species richness using mesoscale environmental variables: model construction and validation for mountain ranges in the Great Basin of western North America. Biological Conservation 110, 21–31.

Marusik, Y.M., Koponen, S., 2002. Diversity of spiders in boreal and arctic zones. Journal of Arachnology 30, 205–210.

Pearson, D.L., Cassola, F., 1992. World-wide species richness patterns of tiger beetles (Coleoptera: Cicindelidae): indicator taxon for biodiversity and conservation studies. Conservation Biology 6, 376–391.

Platnick, N.I., 2004. The world spider catalog, version 4.5. American Museum of Natural History. <http://research.amnh.org/entomology/spiders/catalog81-87/index.html>.

Prendergast, J.R., Eversham, B.C., 1997. Species richness covariance in higher taxa: empirical tests of the biodiversity indicator concept. Ecography 20, 210–216.

Prendergast, J.R., Quinn, R.M., Lawton, J.H., Eversham, B.C., Gibbons, D.W., 1993. Rare species, the coincidence of diversity hotspots and conservation strategies. Nature 365, 335–337.

Reyers, B., Van Jaarsveld, A.S., Kruger, M., 2000. Complementarity as a biodiversity indicator strategy. Proceedings of the Royal Society of London: Biological Sciences 267, 505–513.

Ryti, R.T., 1992. Effect of the focal taxon on the selection of nature reserves. Ecological Applications 2, 404–410.

StatSoft, Inc. 1998. STATISTICA for Windows (Computer program manual). Tulsa, OK, USA.

Van Jaarsveld, A.S., Freitag, S., Chown, S.L., Muller, C., Koch, S., Hull, H., Bellamy, C., Kruger, M., Endrody-Younga, S., Mansell, M.W., Scholtz, C.H., 1998. Biodiversity assessment and conservation strategies. Science 279, 2106–2108.

Williams, P.H., Gaston, K.J., 1994. Measuring more of biodiversity: can higher-taxon richness predict wholesale species richness. Biological Conservation 67, 211–217.